OM protein - protein search, using sw model

GenCore version 4.5
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Run on: March 17, 2001; 20:25:53 ; Search time 77.81 Seconds
(without alignments)
254.443 Million cell updates/sec

Title: US-09-456-306-2
Perfect score: 2985
Sequence: 1 MAHSYAEQLIDTLEAQGVKR..........GGVGAMIDLARSNRINIPTP 579

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Post-processing: Minimum Match 0%
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   A_Geneseq_36:*
             Maximum Match 100%
             Listing first 45 summaries

1: /cgn2_2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /cgn2_2/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /cgn2_2/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /cgn2_2/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /cgn2_2/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /cgn2_2/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /cgn2_2/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /cgn2_2/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /cgn2_2/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /cgn2_2/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /cgn2_2/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /cgn2_2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /cgn2_2/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560.5	18.8	592	9	P80477	Pyruvate oxidase.
2	537.5	18.0	570	11	R09316	Pyruvate oxidase (
3	530.5	17.8	570	11	R05793	Pyruvate oxidase (
4	522.5	17.5	562	18	W22459	E. coli acetolacta
5	517.5	17.3	562	9	P81153	Herbicide sensitiv
6	515	17.3	548	18	W22260	E. coli acetolacta
7	514	17.2	548	17	R88842	E. coli acetolacta
8	514	17.2	548	17	R86881	E. coli 1lvGMEDA o
9	496.5	16.6	548	18	W13731	E. coli threonine-
10	496.5	16.6	669	13	R26618	Protein product of
11	495.5	16.6	669	13	R24798	Ala122 deleted ace
12	495.5	16.6	669	13	R28617	Gly121 deleted ace
13	495.5	16.6	669	13	R28623	Val571 deleted ace
14	495	16.6	666	13	R28616	Amino acids 650-65
15	494.5	16.6	669	13	R28624	Phe578 deleted ace
16	493.5	16.5	669	13	R28622	Asp376 deleted ace
17	493	16.5	669	13	R24800	Ser653 deleted ace
18	493	16.5	670	18	W24457	Arabidopsis wild-t
19	493	16.5	670	19	W59146	A. thaliana acetol
20	493	16.5	670	19	W59147	A. thaliana acetol
21	491.5	16.5	667	13	R28612	Amino acids 255-25
22	488.5	16.4	670	13	R28621	Met351 deleted ace
23	487.5	16.3	665	13	R28614	Amino acids 373-37
24	487.5	16.3	669	13	R28620	Lys256 deleted ace
25	487	16.3	669	13	R28615	Amino acids 569-57
26	486.5	16.3	669	13	R28619	Ala205 deleted ace
27	486	16.3	591	16	R87700	Streptococcus pneu
28	485	16.2	670	12	R11975	Tobacco herbicide-
29	485	16.2	670	13	R26913	ALS mutant of Arap
30	485	16.2	670	16	R63082	Herbicide-resistan
31	485	16.2	577	17	W06554	Arabidopsis herbic
32	484	16.2	664	13	R28613	Arabidopsis herbic
33	482	16.1	666	13	R28609	Amino acids 119-12
34	478	16.0	662	13	R28611	Amino acids 348-35
35	475.5	15.9	658	13	R24801	Amino acids 201-20
36	475.5	15.9	669	13	R24799	Corn acetohydroxy
37	473	15.9	669	13	R28610	R. capsulatus acet
38	461	15.4	594	15	W24464	Prol97/Ser653 dele
39	458	15.3	599	17	R47188	Prol97 deleted ace
40	456	15.3	662	13	W16598	Corn acetohydroxy
41	455	15.2	599	17	R28611	Aceto-hydroxy acid
42	454	15.2	664	18	W16597	Amino acids 194-19
43	453	15.2	599	17	W22455	Corn acetohydroxy
44	452	15.1	666	19	W03692	Amino acids 201-20
44	452	15.1	666	19	W79141	Corn acetohydroxy
45	452	15.1	667	18	W22456	Plant acetolactate

(additional descriptions: R. capsulatus acet / Tobacco wild-type / Corn acetohydroxy / Tobacco wild-type)

ALIGNMENTS

RESULT 1
P80477

ID   P80477 standard; protein; 592 AA.
XX
AC   P80477;
XX
DT   06-NOV-1990 (first entry)
XX
DE   Pyruvate oxidase.
XX
KW   Pyruvate oxidase; ADP; ATP; pyruvic acid.
XX
PN   EP274425-A.
XX
PD   13-JUL-1988.
XX
PF   06-JAN-1988; 88EP-0300073.
XX
PR   15-MAY-1987; 87JP-0118161.
PR   15-MAY-1987; 87JP-0000903.
XX
PA   (TOXN) TOYO JOZO KK.,
XX
PI   Matsumura E, Imamura S, Sagai H, Misaki H, Nogota K;
XX
DR   WPI; 1988-192009/28.
DR   N-PSDB; N81031.
XX
PT   Pyruvate oxidase prepd. by recombinant DNA methods - used for
PT   analysis of pyruvic acid, ADP, ATP or related non-phosphate cpds.
XX
PS   Disclosure; i p; English.
XX
CC   This pyruvate oxidase has no ATPase contamination and can be used for
CC   assaying ADP, ATP, pyruvic acid or other related non-phosphate cpds.

CC   It is produced by recombinant means.
XX
SQ   Sequence   592 AA;

Query Match   18.8%;   Score 560.5; DB 9; Length 592;
Best Local Similarity   29.7%; Pred. No. 1.1e-39;
Matches 154; Conservative 109; Mismatches 235; Indels 21; Gaps 10;

```
Qy    13  LEAQGVKRIYGLVGDSLNPIVDAV--RQSDIEWVHVRNEEAAAFAAGAESLITGELAVCA   70
              |:|:  |||| |  ||:| : ::|:|  :|::||:||||:|  ||| ||| || |:||| |
Db    16  leswgadtiygipsgtlssimdangeeennvkflqvkheevgamaavmqskfggnlgvtv   75

Qy    71  ASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSGYCEMV  130
Db    76  gsgpgashlingiydaamdnipvvailgsrpgrelnmdafqelngnpmydhiavynrrv  135

Qy   131  NGGEQGERILHHAIQSTMAGKGVSVVVIPGDIAK-EDAGDGTYSNSTISSGTPVVFPDPT  189
Db   136  ayaeqlpkivdeearmaiakrgvavievpgdfakveidndqwyssansirkyapiapaaq  195

Qy   190  EAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYIQHENPFE--  247
Db   196  didaavellnnskrpviyagigtmghgpavqelarkikapv--ittgkniefewdfeal  253

Qy   248  VGMSGLLGYGACVDASNEADLILILGTDFPYSD----FLPKDNVAQVDINGAHIGRRTTV  303
Db   254  tgstyrvgwkpanetlieadtvlfagskfpfsevegtfrnvdnfiqididpamlgkrhha  313

Qy   304  KYPVTGDVAATIENILPHVKEKTDRSFLDRMLK--AHERKLSSVVETYTHNVEKHVPIHP  361
Db   314  dvailgdagiaideilnkvdaveesawwtanlknianwreyinmlet--keegdlqfyq  370

Qy   362  EYVASILNELADKDAVFTVDTGMCNVWHARYIE--NPEGTRDFVGSFRHGTMANALPHAIG  420
Db   371  vyna--innhadedaiysidvgnstqtsirhlhmtpknm--wrtsplfatmgiaipgglg  426

Qy   421  AQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKLEMLVEGQPE  480
Db   427  akntypdrqwnligdgafsmntypdvvtvnrynpvinvvfsnteyafiknkyedtnknl  486

Qy   481  FGTDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALA  519
Db   487  fgvdfdvdyakiaeaggakgftvsriedmdrvmaeava  525
```

RESULT   2
R09316
ID   R09316 standard; Protein; 570 AA.
XX
AC   R09316;
XX
DT   15-FEB-1993 (first entry)
XX
DE   Pyruvate oxidase (P178S, A425V).
XX
OS   Synthetic.
XX
KW   POD; mutation; decarboxylation; assay.
XX
FH   Key   Location/Qualifiers
FH
FT   Misc-difference 178
FT   /label= mutation
FT   /note= "Pro -> Ser; at least one of wild-type
FT   Pro178 and Ala425 is exchanged for
FT   Ser178 and Val425"
FT   Misc-difference 425
FT   /label= mutation
FT   /note= "Ala -> Val; at least one of wild-type
FT   Pro178 and Ala425 is exchanged for
FT   Ser178 and Val425"
XX
PN   DE3833601-A.

XX
PD   05-APR-1990.
XX
PF   03-OCT-1988;   88DE-3833601.
XX
PR   03-OCT-1988;   88DE-3833601.
XX
PA   (BOEF) BOEHRINGER MANNHEIM GMBH.
XX
PI   Mollering H, Schumacher G;
XX
DR   WPI; 1990-108586/15.
DR   N-PSDB; Q08597.
XX
PT   New-stable, mutated forms of pyruvate oxidase - having specific
PT   aminoacid substitutions, useful as assay reagents, are encoded in
PT   new DNA
XX
PS   Claim 2; Page 5; 10pp; German.
XX
CC   The DNA sequence of wild-type POD, given in Q03827, may be mutated so
CC   that at least 178-Pro and/or 425-Ala of the encoded POD are exchanged.
CC   This may be achieved by mutation of nucleotides 532, 533, 534, 1273,
CC   1274 and/or 1275.
CC   For example, the sequence given below comprises mutations of
CC   nucleotides 532 and 1274 from C to T, resulting in exchange from
CC   178-Pro to Ser and 425-Ala to Val.
CC   The mutated pyruvate oxidase (POD) decarboxylates pyruvate with
CC   formation of H202 and is active without addn. of FAD, thiamine
CC   pyrophosphate and divalent metal ions. It is more stable (esp. in
CC   presence of salts and at alkaline pH) than wild-type enzyme, and is
CC   better suited for assay of pyruvate, or pyruvate-generating reactions.
XX
SQ   Sequence   570 AA;

Query Match   18.0%;   Score 537.5; DB 11; Length 570;
Best Local Similarity   26.6%; Pred. No. 9.8e-38;
Matches 142; Conservative 113; Mismatches 227; Indels 51; Gaps 9;

```
Qy     9  LIDTLEAQGVKRIYGLVGDSLNPIVDAV--RQSDIEWVHVRNEEAAAFAAGAESLITGEL   66
Db    17  vikvleawgvdhiygipgsinsimdalsaerdrihyiqvrheevganaaaadakltgki   76

Qy    67  AVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSGY  126
Db    77  gvcfgsagpggthlimngiydaredhvpvlaliggfgttgmnmdtfqennenplyadvady  136

Qy   127  CEMVNGGEQGERILHHAIQSTMAGKGVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVVFP  186
Db   137  nvtavnaatiphvideairrayahggvavvqipvdlpwqq------isaerpli--  184

Qy   187  DPTEAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYIQHENPF  246
Db   185  ------------yygigaxkagkeleqlskstkiplmstypakqivadrypa  224

Qy   247  EVGMSGLLGYGACVDASNEADLILILGTDFPYSD----FLPKDNVAQVDINGAHIGRRTT  302
Db   225  yigsanrvaqkpaneaiaqadvvlfvgnnypfaevskafkntryflqididpaklgkrhk  284

Qy   303  VKYPVTGDVAATIENILPHVKEKTDRSFLDRML---KAHERKLSSVVETYTHNVEKHVPI  359
Db   285  tdiavladagktlaailaqvserestpwwqanlanvknwraylasled------kqeppl  338

Qy   360  HPEYVASILNELADKDAVFTVDTGMCNVWHARYIENPEGTRDEVGSFRHGTMANALPHAI  419
Db   339  qayavlravnkiaepdalysivgdinlnanrhlkltpsnrhitsnl-fatmvgipgai  397

Qy   420  GAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKLEMLVEGQP  479
Db   398  aaklnyperqvfnlagdggasmtmqdlvtqvgyhlpvinvvftncqyyfikdeqedtnqn  457

Qy   480  EF-GTDHEEVNFAEIAAAAGIKSVRITDPKKVRE--QLAEALAYPGPVLIDIV  529
```

```
Db   458 dfigvefndidfskiadgvhmqafrvnkieqlpdvfegakaiaghepvlidav 510
           :|:.||:||| :|:::||| :|                :||||||
```

RESULT   3

```
ID     R05793 standard; Protein; 570 AA.
XX
AC     R05793;
XX
DT     15-FEB-1993 (first entry)
XX
DE     Pyruvate oxidase (wild-type).
XX
KW     POD; mutation; decarboxylation; assay.
XX
OS     Synthetic.
XX
PN     DE3833601-A.
XX
PD     05-APR-1990.
XX
PF     03-OCT-1988; 88DE-3833601.
XX
PR     03-OCT-1988; 88DE-3833601.
XX
PA     (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI     Mollering H, Schumacher G;
XX
DR     WPI; 1990-108586/15.
DR     N-PSDB; O03827.
XX
PT     New stable, mutated forms of pyruvate oxidase - having specific
PT     aminoacid substitutions, useful as assay reagents, are encoded in
PT     new DNA
XX
PS     Claim 15; Page 6; 10pp; German.
XX
CC     The sequence of wild-type POD, given below, may be mutated so
CC     that at least 178-Pro and/or 425-Ala are exchanged.
CC     Esp. the mutation is from 178-Pro to Ser and/or 425-Ala to Val.
CC     The mutated pyruvate oxidase (POD) decarboxylates pyruvate with
CC     formation of H2O2 and is active without addn. of FAD, thiamine
CC     pyrophosphate and divalent metal ions. It is more stable (esp. in
CC     presence of salts and at alkaline pH) than wild-type enzyme, and is
CC     better suited for assay of pyruvate, or pyruvate-generating reactions.
CC     See also Q08597.
XX
SQ     Sequence   570 AA;
```

```
Query Match       17.8%; Score 530.5; DB 11; Length 570;
Best Local Similarity  26.5%; Pred. No. 3.9e-37;
Matches 141; Conservative 112; Mismatches 229; Indels 51; Gaps 9;

Qy     9 LIDTLEAGVKRIYGLVGDSLNPIVDAV--RQSDIEWVHVRNEEAAFANAGAESLITGEL 66
           |  |  || |  |   |  || .| |   |:| ||  | |||  .|| .   .| |
Db    17 vlkvleewgvdhiyglpggsinsimdalsaerdrihylgvrheevgamaaadak1tgki 76

Qy    67 AVCAASCGPGNTHLIQGLYDSHRNCAKVLAIASHIPSAQIGSTFFQETHPEILFKECSGY 126
          |:| ||| |||  | ||| ||   ||  |  | ||   :|    |||:|:  | | | |
Db    77 gvcfgsagpggthlmglydaredhvpvlaliggfgttgmnndtfqemnenplyadvady 136

Qy   127 CEMVNGGEQGER1LHHIATOSTMAGKGVSVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVVFP 186
           |   | |    || :        |||| |||| :| | | :        || |   ::: :| |
Db   137 nvtavnaatlphvideairrayahggvavvqipvdlpwqq-------ipaerpli-- 184

Qy   187 DPTEAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYIQHENPF 246
             |        |       ||   |  |    |  |||  ||| :   :   || ||  :||  |
Db   185 --------------------yygigarkagkeleqlsktklkiplmstypakgivadrypa 224

Qy   247 EVGMSGLLGYGACVDASNEADLLILLGTDFPYSD----FLPKDNVAQVDINGAHIGRRTT 302
```

```
Db   225 ylgsanrvaqkpaneaiaqadvvlfvgnnyphaevskafkntryflqidididpaklgrkhk 284
             :|        :      | |. :|| |:|  .  :|  |    .     : .|::|.| :
Qy   303 VKYPVTGDVAATIENLLPHVKEKTDRSFLDRML---KAHERKLSSVVETYTINVEKIHVPI 359
           |: |    ||:   :     :      |:|.|           | .:|  .  ::|: .:   ||
Db   285 tdiavladagktlaallaqvserestpvwqanlanvknwrayiasled------kqegpl 338

Qy   360 HPEYVASILNELADKDAVFTVDTGMCNVWHARYIENPEGTRDFVGSFRHGTMANALPHAI 419
            :| :|| :| |  :|| :  |:  |..    |   ||  || |:|. |  | .   ||.| | |
Db   339 qayqvlravnkiaepdaiysidvgdnlnanrhiklipsnrhitsnl-fatmgvglppgal 397

Qy   420 GAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKLEMLVECQP 479
           || |  :|:|::   |||| |:|| |||  |:  |:|    ||:| || |.  |  |  .||:
Db   398 aaklnyperqyfnlagdgggasintmqdiatqvqyhlpvinvvftncqyqfikdeqedtnqn 457

Qy   480 EF-GTDHEEVNFAEIAAAAGIKSVRITDPKKVRE--QLAEALAYPGPVLIDIV 529
           || |||::   || :|    :|| .|:  | |  |:     | .    ||| |:|:
Db   458 dfigvefndidfskiadgvhmqafrvnkieqlpdvfegakaiaghepvlidav 510

Qy       Sequence   570 AA;
```

RESULT   4

```
ID     W22459 standard; Protein; 562 AA.
XX
AC     W22459;
XX
DT     25-SEP-1997 (first entry)
XX
DE     E. coli acetolactate synthase isozyme I (sub-sequence E).
XX
KW     Acetolactate synthase; ALS; herbicide resistance; transgenic plant;
KW     crop protection.
XX
OS     Escherichia coli.
XX
DR     US5605011-A.
XX
PN     US5605011-A.
XX
PD     25-FEB-1997.
XX
PF     26-AUG-1986; 86US-0900609.
XX
PR     27-JUL-1987; 87IL-0083348.
XX
PA     (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI     Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
PI     Yadav NS;
XX
DR     WPI; 1997-153232/14.
XX
PT     Use of mutant acetolactate synthase genes - for transforming plants
PT     for resistance to sulphonylurea, triazolopyrimidine sulphonamide
PT     and imidazolinone herbicides.
XX
PS     Claim 1; Fig 6a-f; 63pp; English.
XX
CC     Amino acid sub-sequences A-G respectively correspond to the large
CC     subunits of acetolactate synthase (ALS) isozymes I, II and III
CC     (W22459-61) from E. coli, and wild-type ALS proteins of yeast
CC     (W22458), Arabidopsis thaliana (W22457) and tobacco (W22455 and
CC     W22456).  Comparison of these substantially conserved sequences
CC     with those of herbicide-resistant ALS enzymes (see also W22462-64)
CC     reveals the location of amino acid substns. that lead to herbicide
CC     resistance.  In sub-sequence E, such a substn. is located at the
CC     gamma-1 position (any amino acid other than aspartate acid).  A
CC     nucleic acid encoding an ALS from any source can be mutated so that
CC     the encoded enzyme contains this amino acid substn.  Transformation
CC     of herbicide sensitive plants or plant cells with the nucleic acid
CC     results in resistance to the herbicide.
XX
SQ     Sequence   562 AA;
```

```
Qy   480 EF-GTDHEEVNFAEIAAAAGIKSVRITDPKKVRE--QLAEALAYPGPVLIDIV 529
Db   398 aaklnyperqyfnlagdgggasintmqdiatqvqyhlpvinvvftncqyqfikdeqedtnqn 457

Qy   458 dfigvefndidfskiadgvhmqafrvnkieqlpdvfegakaiaghepvlidav 510
Db   458 dfigvefndidfskiadgvhmqafrvnkieqlpdvfegakaiaghepvlidav 510
```

Left column (RESULT 5)

Query Match   17.5%; Score 522.5; DB 18; Length 562;
Best Local Similarity   28.1%; Pred. No. 1.9e-36;
Matches 163; Conservative 107; Mismatches 239; Indels 71; Gaps 17;

```
Qy    6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQS-DIEWVHVRNEEAAAFAAGAESLITG 64
          :|| |:|| ||:|  ||:||||  | | :| | ::   ::|  |  |  ||| :|  |
Db   16 aefivhfleqggikivtgipggsilpvydalsqstqirhllarheggagfiaqgmartdg 75

Qy   65 ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFQETHPEILFKECS 124
          ||| | | ||| ||| :     |  |  | |  | :|  ||| :      |  | :
Db   76 kpavcmacsgppgatnlvtaiadarldsiplicitgqvpasmigtdafqevdtygisipit 135

Qy  125 GYCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDI-------------AKEDAGDGT 171
          |  :|:   |:|  :  :|  |: |   |:|:::|| :              || |  :
Db  136 khnylvrhieelpqvmsdafriaqsgrppgpwididpkdvqtavfeietqpamaekaaapa 195

Qy  172 YSNSTISSGTPVVFPDPTEAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIG 231
           :  :| |     |: ||  |  :| ||| |  |  ||| :|  |:|:|||| ||: :
Db  196 fseesi----------rdaaam----inaakrpvlylgggvinaparvrelaekaqiptt 241

Qy  232 HAIGGKQYIQHENPFEVGMSGLLGYGACVDASNEADLILLLGTDF------PYSDFLPKD 285
           :   :| | :   |||||||| | ::| : :||| :|::||| |      ||||:  :
Db  242 mtlmalgmlpkahplsigmlgmhgvrstnyilqeadllivlgarfddraigkteqfcpna 301

Qy  286 NVAQVDINGAHIGRRTTVKYP---VTGDVAATIENILPHVKEKTDRSFLDRMLKAHERK- 341
          |:  ||::  || |  |  :    | ||| | |||  |:  :|  | | | : ::| :
Db  302 kiihvdidraqigk----ikqphvaiqadvddvlaqliplv-eaqpraewhqivadiqref 357

Qy  342 ---LSSVVETYTHNVEKHVPHPEYVASILNELA---DKDAVFTVDGTDGMCNVWHARY--I 393
             |||| |  ||| ::||: |  |:|:||| |    : :   |||  ||| :|||:  |
Db  358 ----------ygllinavaacvddnaiittdvgqhqmwtaqaypl 404

Qy  394 ENPEGTRDFVGSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQ 453
           ||  ||||||| |:||||||| |||:| :|  |:|:|::|||| |||::||||||||||
Db  405 nrp---rqwltsgglgtmgfglpaatgaalanpdrkvlcfsgdgslmmniqematastenq 461

Qy  454 LPLKAVVFNNSSLGMV-KLEMLVEGQPEF-GTDHEEVNFAEIAAAAGIKSVRITDPKKVR 511
          |:|||||:||| ||:  ||:|| |||  | || |||:|| :||||| ||::|:||| |:
Db  462 ldvkilimnnealglvhqqgslfyeggafvatypgkinfmqiaagfgletcdinneadpq 521

Qy  512 EQLAEALAYPGPVLIDIVTDPNAL---SIPPITTWEQVMG 548
          : | |:| ||| :|: :  ||| |   |||:||||:|:|
Db  522 asiqelinrpgpalihvridaeekvpmvppgaantemvg 561
```

RESULT 5
P81153   5
ID   P81153 standard; protein; 562 AA.
XX
AC   P81153;
XX
DT   17-OCT-1990 (first entry)
XX
DE   Herbicide sensitive, wild type ALS.
XX
KW   Tobacco; C3 mutant; SURA; acetolactase synthase; sulphonylurea herbicide.
XX
OS   Arabidopsis thaliana.
XX
PN   EP257993-A.
XX
PD   02-MAR-1988.
XX
PF   20-AUG-1987; 87EP-0307384.
XX
PR   26-AUG-1986; 86US-0900609.
XX
PA   (DUPO) DU PONT DE NEMOURS CO.
XX
PI   Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Yadav NS;
XX
DR   WPI; 1988-058164/09.
XX

Right column (RESULT 6)

PT   New nucleic acid fragment coding - for mutant aceto-lactate
PT   synthetase resistant to sulphony1-urea herbicides, and
PT   transformed resistant crop plants.
XX
PS   Disclosure; ; p; English.
XX
CC   The sequence is that of the wild type herbicide sensitive form of ALS
CC   encoded by the SURA gene.
CC   See also P81149-55.
XX
SQ   Sequence 562 AA;

Query Match   17.3%; Score 517.5; DB 9; Length 562;
Best Local Similarity   27.9%; Pred. No. 5e-36;
Matches 162; Conservative 107; Mismatches 240; Indels 71; Gaps 17;

```
Qy    6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQS-DIEWVHVRNEEAAAFAAGAESLITG 64
          :|| |:|| ||:|  ||:||||  | | :| | ::   ::|  |  |  ||| :|  |
Db   16 aefivhfleqggikivtgipggsilpvydalsqstqirhllarheggagfiaqgmartdg 75

Qy   65 ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFQETHPEILFKECS 124
          ||| | | ||| ||| :     |  |  | |  | :|  ||| :      |  | :
Db   76 kpavcmacsgppgatnlvtaiadarldsiplicitgqvpasmigtdafqevdtygisipit 135

Qy  125 GYCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDI-------------AKEDAGDGT 171
          |  :|:   |:|  :  :|  |: |   |:|:::|| :              || |  :
Db  136 khnylvrhieelpqvmsdafriaqsgrppgpwididpkdvqtavfeietqpamaekaaapa 195

Qy  172 YSNSTISSGTPVVFPDPTEAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIG 231
           :  :| |     |: ||  |  :| ||| |  |  ||| :|  |:|:|||| ||: :
Db  196 fseesi----------rdaaam----inaakrpvlylgggvinaparvrelaekaqiptt 241

Qy  232 HAIGGKQYIQHENPFEVGMSGLLGYGACVDASNEADLILLLGTDF------PYSDFLPKD 285
           :   :| | :   |||||||| | ::| : :||| :|::||| |      ||||:  :
Db  242 mtlmalgmlpkahplsigmlgmhgvrstnyilqeadllivlgarfddraigkteqfcpna 301

Qy  286 NVAQVDINGAHIGRRTTVKYP---VTGDVAATIENILPHVKEKTDRSFLDRMLKAHERK- 341
          |:  ||::  || |  |  :    | ||| | |||  |:  :|  | | | : ::| :
Db  302 kiihvdidraqigk----ikqphvaiqadvddvlaqliplv-eaqpraewhqivadiqref 357

Qy  342 ---LSSVVETYTHNVEKHVPHPEYVASILNELA---DKDAVFTVDGTDGMCNVWHARY--I 393
             |||| |  ||| ::||: |  |:|:||| |    : :   |||  ||| :|||:  |
Db  358 ----------ygllinavaacvddnaiittdvgqhqmwtaqaypl 404

Qy  394 ENPEGTRDFVGSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQ 453
           ||  ||||||| |:||||||| |||:| :|  |:|:|::|||| |||::||||||||||
Db  405 nrp---rqwltsgglgtmgfglpaatgaalanpdrkvlcfsgdgslmmniqematastenq 461

Qy  454 LPLKAVVFNNSSLGMV-KLEMLVEGQPEF-GTDHEEVNFAEIAAAAGIKSVRITDPKKVR 511
          |:|||||:||| ||:  ||:|| |||  | || |||:|| :||||| ||::|:||| |:
Db  462 ldvkilimnnealglvhqqgslfyeggafvatypgkinfmqiaagfgletcdinneadpq 521

Qy  512 EQLAEALAYPGPVLIDIVTDPNAL---SIPPITTWEQVMG 548
          : | |:| ||| :|: :  ||| |   |||:||||:|:|
Db  522 asiqelinrpgpalihvridaeekvpmvppgaantemvg 561
```

RESULT 6
W22460   6
ID   W22460 standard; protein; 548 AA.
XX
AC   W22460;
XX
DT   25-SEP-1997 (first entry)
XX
DE   E. coli acetolactate synthase isozyme II (sub-sequence F).
XX
KW   Acetolactate synthase; ALS; herbicide resistance; transgenic plant;
KW   crop protection.
XX
OS   Escherichia coli.
XX

PN   US5605011-A.
XX
PD   25-FEB-1997.
XX
PF   26-AUG-1986;   86US-0000609.
XX
PR   27-JUL-1987;   87IL-0083348.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Yadav NS;
PI   Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
XX
DR   WPI; 1997-153232/14.
XX
PT   Use of mutant acetolactate synthase genes - for transforming plants
PT   for resistance to sulphonylurea, triazolopyrimidine sulphonamide
PT   and imidazolinone herbicides.
XX
PS   Claim 1: Fig 6a-f: 63pp; English.
XX
CC   Amino acid sub-sequences A-G respectively correspond to the large
CC   subunits of acetolactate synthase (ALS) isozymes I, II and III
CC   (W22459-61) from E. coli, and wild-type ALS proteins of yeast
CC   (W22455), Arabidopsis thaliana (W22457) and tobacco (W22456).
CC   (W22456). Comparison of these substantially conserved sequences
CC   with those of herbicide-resistant ALS enzymes (see also W22462-64)
CC   reveals the location of amino acid substns. that lead to herbicide
CC   resistance. In sub-sequence F, such substns. are located at the
CC   beta-3 (any amino acid other than tryptophan) and beta-7 (any
CC   amino acid other than phenylalanine) positions. A nucleic acid
CC   encoding an ALS from any source can be mutated so that the encoded
CC   enzyme contains these amino acid substns. Transformation of
CC   herbicide sensitive plants or plant cells with the nucleic acid
CC   results in resistance to the herbicide.
XX
SQ   Sequence 548 AA;

Query Match   17.3%;   Score 515;   DB 18;   Length 548;
Best Local Similarity   30.1%;   Pred. No. 7.9e-36;
Matches 164;   Conservative 91;   Mismatches 249;   Indels 40;   Gaps 13;

Qy   6 AEQLIDFLEAQGVKRIYGLVGDSLNPIVDAVRQSDIEWVHVRNEEAAAFAAGAESLITGE   65
          :|||| ||| ::| |||||||||||||||||||||||||||||||||||||||||||
Db   4 aqwvvhalraggvntvfgypggaimpvydalydggvehllcrheggaamaalgyaratgk   63

Qy   66 LAVCAASCGPGNTHLIQGLYDSIIRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSG 125
          | | :| |:| || ||:|||| | :| :| :| | ::|: ||:| | :: |:
Db   64 tgvclatsgpgatnlltgliadalldslpvvaltgqvsapflgtdafqevdviglslactk 123

Qy   126 YCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVV 184
          | : : ||:| || |:: | ::| ||||| : | | | : |:|: || :|:|
Db   124 hsflvqsleelprimaeafdvacsgrppqpvldvlipkdi-qlasgdlepwfltven--evt 180

Qy   185 FPDPTEAAALVEAINNAKSVTLFCGAGVKNARA--QVELEAEKIKSPIGHALGGKQYIQH 242
          || | | | |:: | ||:| :| | : || : | : ::|: || : | ||| |
Db   181 fph-aeveqarqmlakaqkpmlyvggvgvgmaqavpalreflaatkmpatctlkglgavea 239

Qy   243 ENPFEVGMSGLLGYGACVDASNEADLLLLGTDF------PYSDFLPKDNVAQVDINGAH 296
          ||| : | || || ||: |:|| | |||| | |:: | || | |||| |
Db   240 dyppylgmlgmhgtkaanfavgeecdlllavgarfddrvtgkintfaphasvlhmdidpae 299

Qy   297 IGRRTTVKYPVTGCDVAATIENILPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNVEKH 356
          ||| | | | ||:|| ||||| |: |:||| || || ||:|| : | |::|:|
Db   300 mnklrqahvalqgdinallpalqqplnqydwdqhcaqlrdehswr------ydh----- 347

Qy   357 VPIIPEVVASILNELADK---DAVFTVDTGMCNVWHARYIEN--PEGTRDPVGSFRIGTM 411
          |: | ||| : || | |:|: | ||| :: ||| |: || ||:| :| :|| |
Db   348 -pgdalyaplilkqlsdrkpadcvvtcdvghqhmwaaghlahtrpe---nfltssg1gtm 403

Qy   412 ANALPIHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKL 471
          || | | ||||: || |:: | ||||| ||| :||| | || |:||:||| ||::
Db   404 gfglpaavgaqvarpndtvvcisgdgsfmmnvqelgtvkrkqplpklv1ldnqrlgmvrq 463

Qy   472 EMLVEGQPEFG-----TDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYPGPVLID 527
          : :| || | || : | | ||||| :|||| :|: | | || ||||
Db   464 wqgilffqerysettltdnpd--fimlasafglhgqhltrkdqveaaldtminsdppyllh 521

Qy   528 IVTD 531
          | |
Db   522 vsid 525

RESULT   7

R88842

ID   R88842 standard; Protein; 548 AA.
XX
AC   R88842;
XX
DT   08-OCT-1996 (first entry)
XX
DE   E. coli ilvGMEDA operon ilvG, ilvM, ilvE and ilvD gene protein prod.
XX
KW   ilvGMEDA operon; modification; ilvG; ilvM; ilvE; ilvD; ilvA;
KW   threonine deaminase; L-Valine; L-isoleucine; L-leucine; repression;
KW   transformation; bacterial host; lipoic acid; H+-ATPase deficient;
KW   production; high yield.
XX
OS   Escherichia coli.
XX
PN   WO9606926-A1.
XX
PD   07-MAR-1996.
XX
PF   30-AUG-1995;   95WO-JP01719.
XX
PR   30-AUG-1994;   94JP-0204856.
XX
PA   (AJIN) AJINOMOTO CO INC.
XX
PI   Hashiguchi K, Ishigooka M, Kurahashi O, Tomita F;
PI   Yokota A;
XX
DR   WPI; 1996-160357/16.
DR   N-PSDB; T12801.
XX
PT   Efficient microbial prodn. of L-valine and L-leucine - by culturing
PT   Escherichia strain which requires lipoic acid for growth and/or is
PT   deficient in H+-ATPase.
XX
PS   Claim 8; Pages 31-36; 5pp; Japanese.
XX
CC   The present sequence is the protein prod. of the E. coli ilvGMEDA
CC   operon, which has be modified to express only the ilvG, ilvM, ilvE
CC   and ilvD genes, but not the ilvA (threonine deaminase) gene, which
CC   is required for L-Valine, L-isoleucine and/or L-leucine repression.
CC   The modified operon can be used to transform a bacterial host, esp.
CC   E. coli, which requires lipoic acid for growth and/or is deficient
CC   in H+-ATPase, for the efficient prodn. of L-valine and L-leucine
CC   in high yield. A specific example is the transformed H+-ATPase
CC   deficient E. coli strain W1485atpA401/pMWdAR6, which when cultured
CC   in 1 microg/L lipoic acid at 37 degrees C for 24 hrs. gave 8.0 g/L
CC   L-Valine in the medium, compared to 0.1 g/L for the untransformed
CC   strain.
XX
SQ   Sequence 548 AA;

Query Match   17.2%;   Score 514;   DB 17;   Length 548;
Best Local Similarity   30.1%;   Pred. No. 9.6e-36;
Matches 164;   Conservative 91;   Mismatches 249;   Indels 40;   Gaps 13;

Qy   6 AEQLIDFLEAQGVKRIYGLVGDSLNPIVDAVRQSDIEWVHVRNEEAAAFAAGAESLITGE   65
          :|||| ||| ::| |||||||||||||||||||||||||||||||||||||||||||
Db   4 aqwvvhalraggvntvfgypggaimpvydalydggvehllcrheggaamaalgyaratgk   63

```
Qy    66  LAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSG 125
          |||:| |||| ::|| |||:|:||| :|| || |:|| |||| || | |: :|||| |||
Db    64  tgvciatsgpgatniltgladalldsipvvaitgqvsapfigtdafgevdvlglslactk 123

Qy   126  YCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVV 184
          ::|:| | | |   : :|| :|  |: ||::|:||||:  :  :||:  | ::|:|||:
Db   124  hsflvqsleelprimaeafdvacsgrppgpvlvdipkdl-qlasgdlepwfttven--evt 180

Qy   185  FPDPTEAAALVEAINNAKSVTLFCGAGVKNARA--QVLELAEKIKSPIGHALGGKQYIQH 242
          ||   ||  ::| :|| ||  : ||.|| :.|  ||:| |:  :  | || ||| ||
Db   181  fph-aeveqarqmlakaqkpmlyvggvgvgmaqavpalrefiaatkmpatctlkglgavea 239

Qy   243  ENPFEVGMSGLLGYGACVDASNEADLLILLGTDF-----PYSDFLPKDNVAQVDINGAH 296
          ::| :: || ||: :: | |:| | ||| |||    |:  ||  |::| ||: |
Db   240  dyppyylgmlgmhgtkaanfavqecdlliavgarfddrvtgklntfaphasvihmdidpae 299

Qy   297  IGRRTTVKYPVTGDVAATIENLLPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNVEKH 356
          :| : ::|  ||| ::| :||||  :   :  | |  |:|| | : || :::  |
Db   300  mnklrqahvalggdlnallpalqgplngcdwqghcaqirdehswr----ydh----- 347

Qy   357  VPIHPEYVASILNELADK---DAVFTVDTGMCNVWHARYIEN--PEGTRDFVGSFRHGTM 411
          :| :  :||:|::|| |:     | |||:||  |  : |:  :  | :|:|||| | ||
Db   348  -pgdaiyapllikqlsdrkpadcvvtdvgqhqmwaaqhiahtrpe---nfitssqlgtm 403

Qy   412  ANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKL 471
          .. ||  | ||.| || || : ||||  || : | | || ||:|||:|:::|: |||::
Db   404  gfglpaavgaqvarpndtvvcisgdgsfmmnvqelgtvkrkqlplkivlldnqrlgmvrq 463

Qy   472  EMLVEGQPEFG---TDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYPGPVLID 527
          |: | || |:     |:|  ::: |:|  | ||: | |:|  |:|:| |:: :| |:||
Db   464  wqqlffqqrysettltdnpd--flmlasafgihgqhitrkdqveaaldtmlnsdppyllh 521

Qy   528  IVTD 531
          :| |
Db   522  vsid 525
```

RESULT   8
R86881
ID   R86881 standard; protein; 548 AA.
XX
AC   R86881;
XX
DT   15-OCT-1995 (first entry)
XX
PR   30-MAY-1994; 94JP-0116340.
XX
PF   30-MAY-1994; 95EP-0108315.
XX
PD   06-DEC-1995.
XX
PN   EP685555-A1.
XX
OS   Escherichia coli.
XX
KW   enzyme; metabolic engineering; L-isoleucine; feedback-inhibition.
KW   aspartokinase-I; homoserine-dehydrogenase I; threonine-deaminase;
KW   thrABC operon; ilvGMEDA operon; thrA gene; ilvA gene; amino acid;
DE   E. coli threonine-deaminase.
XX
PA   (AJIN) AJINOMOTO CO INC.
XX
PI   Hashiguchi K, Kishino H, Matsui H, Tsujimoto N;
XX
DR   WPI; 1996-012380/02.
DR   N-PSDB; T07115.
XX
PT   New Escherichia transformant producing L-isoleucine - carrying thr
PT   ABC operon, ilv GMEDA operon and opt. Lys C gene, all of which are
PT   released from feedback inhibition

PS   Disclosure; Page 35-38; 48pp; English;
XX
CC   This sequence is encoded by an E. coli ilvGMEDA operon which comprises
CC   a ilvA gene coding for threonine-deaminase. This enzyme is released
CC   from inhibition by L-isoleucine, during fermentation of E. coli for
CC   the production of L-isoleucine.
XX
SQ   Sequence   548 AA;

Query Match   17.2%; Score 514; DB 17; Length 548;
Best Local Similarity   30.1%;   Pred. No. 9.6e-36;
Matches 164; Conservative   91; Mismatches 249; Indels   40; Gaps 13;

```
Qy     6  AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQSDIEWVHVRNEEAAAFAAGAESLITGE 65
          |:|:  |:||.||  : :| | |  |:|:|: :  ::::| : |:|:||:||:::| ||
Db     4  agwvhalraggvntvfgyppggaimpvydaliyddggvehllcrheqgaamaaiqyaratgk 63

Qy    66  LAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSG 125
          |||:| |||| ::|| |||:|:||| :|| || |:|| |||| || | |: :|||| |||
Db    64  tgvciatsgpgatniltgladalldsipvvaitgqvsapfigtdafgevdvlglslactk 123

Qy   126  YCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVV 184
          ::|:| | | |   : :|| :|  |: ||::|:||||:  :  :||:  | ::|:|||:
Db   124  hsflvqsleelprimaeafdvacsgrppgpvlvdipkdl-qlasgdlepwfttven--evt 180

Qy   185  FPDPTEAAALVEAINNAKSVTLFCGAGVKNARA--QVLELAEKIKSPIGHALGGKQYIQH 242
          ||   ||  ::| :|| ||  : ||.|| :.|  ||:| |:  :  | || ||| ||
Db   181  fph-aeveqarqmlakaqkpmlyvggvgvgmaqavpalrefiaatkmpatctlkglgavea 239

Qy   243  ENPFEVGMSGLLGYGACVDASNEADLLILLGTDF-----PYSDFLPKDNVAQVDINGAH 296
          ::| :: || ||: :: | |:| | ||| |||    |:  ||  |::| ||: |
Db   240  dyppyylgmlgmhgtkaanfavqecdlliavgarfddrvtgklntfaphasvihmdidpae 299

Qy   297  IGRRTTVKYPVTGDVAATIENLLPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNVEKH 356
          :| : ::|  ||| ::| :||||  :   :  | |  |:|| | : || :::  |
Db   300  mnklrqahvalggdlnallpalqgplngcdwqghcaqirdehswr----ydh----- 347

Qy   357  VPIHPEYVASILNELADK---DAVFTVDTGMCNVWHARYIEN--PEGTRDFVGSFRHGTM 411
          :| :  :||:|::|| |:     | |||:||  |  : |:  :  | :|:|||| | ||
Db   348  -pgdaiyapllikqlsdrkpadcvvtdvgqhqmwaaqhiahtrpe---nfitssqlgtm 403

Qy   412  ANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKL 471
          .. ||  | ||.| || || : ||||  || : | | || ||:|||:|:::|: |||::
Db   404  gfglpaavgaqvarpndtvvcisgdgsfmmnvqelgtvkrkqlplkivlldnqrlgmvrq 463

Qy   472  EMLVEGQPEFG---TDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYPGPVLID 527
          |: | || |:     |:|  ::: |:|  | ||: | |:|  |:|:| |:: :| |:||
Db   464  wqqlffqqrysettltdnpd--flmlasafgihgqhitrkdqveaaldtmlnsdppyllh 521

Qy   528  IVTD 531
          :| |
Db   522  vsid 525
```

RESULT   9
W13731
ID   W13731 standard; protein; 548 AA.
XX
AC   W13731;
XX
DT   24-NOV-1997 (first entry)
XX
DE   Protein product of Escherichia coli ilvG gene open reading frame 2.
XX
KW   ilvG; L-isoleucine; production; open reading frame 2; ORF2.
XX
OS   Escherichia coli.
XX
PN   WO9708333-A1.
XX
PD   06-MAR-1997.
XX

```
PF   27-AUG-1996;   96WO-JP02399.
XX
PR   30-JUL-1996;   96JP-02008060.
PR   30-AUG-1995;   95JP-0221561.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Ito H, Izui M, Kishino H, Kurahashi O, Ono Y;
XX
DR   WPI; 1997-179289/16.
DR   N-PSDB; T62750.
XX
PS   Example 5; Pages 26-31; 41pp; Japanese.
XX
PT   Production of L-amino acids (phenylalanine etc) by microbial culture
PT   - using microorganisms such as Escherichia or Corynebacterium having
PT   an enhanced ability to produce phospho:enol:pyruvic acid
XX
CC   The present sequence is the protein product of the Escherichia coli
CC   ilvG gene open reading frame 2, which is involved in the production
CC   of L-isoleucine.
XX
SQ   Sequence   548 AA;

Query Match     17.2%;   Score 514;   DB 18;   Length 548;
Best Local Similarity     30.1%;   Pred. No. 9.6e-36;
Matches 164;   Conservative 91;   Mismatches 249;   Indels 40;   Gaps 13;

Qy      6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQSDIEWVHVRNEEAAAFAAGAESLITGE 65
            :||  | |||   | :|||:|    ||    :||::  |   ::     |   :  :
Db      4 aqwvvhalraqgvntvfgypggaimpvydalyqggvehllcrheqggamaaigyaratgk 63

Qy     66 LAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSG 125
            | |:|:|||| |||| |  || ||:| |:| :    ::|   :||: :|  |   |  ||
Db     64 tgvclatsgpgathlltgladalldsipvvaltgqvsapfigtdafqevdvigislackt 123

Qy    126 YCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVV 184
             :  : |  ::|  | ::  ::  |   ||:|: :|      :  | :::  ||   ||
Db    124 hafivqsleelprimaeafdvacsgrppvvldlpkdl-qlasgdlepwfttven--evt 180

Qy    185 FPDPTEAAALVEAINNAKSVTLFCGAGVKNARA--QVLELAEKIKSPIGHALGGKQYIQH 242
            |    :   |:||   ||:    ||| |  | |   |: |||:|  |   | ||: :|
Db    181 fph-aevegarqmlakaqkpmljyvqggvgmaqavpairefllaatkmpatctlkglgavea 239

Qy    243 ENPFEVGMSGLLGYGACVDASNEADLLILLGTDF------PYSDFLPKDNVAQVDINGAH 296
            :  :  ||  :  | || :   : :||:: |:||       |  :    :|  :||  |
Db    240 dypylgmlgmhgtkaeanfavqecdlliavgarfddrvtgkintfaphasvimdidpae 299

Qy    297 IGRRTTVKYPVTGDVAATIENLLPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNVEKH 356
            :  :  ::       :  :  :|   :   ||  :  ::  | :::   :   ||
Db    300 mnkilrqahvalqgdinallpalqqplnqcdwqqhcaqlrdehswr------ydh---- 347

Qy    357 VPIHPEYVASILNELADK---DAVFTVDTGMCNVWHARYIEN--PEGTRDFVGSFRHGTM 411
            :| : |  :::::: |     ||:  : |   | : | :|:    :  :|:  |  : |
Db    348 -pgda.yapl.likqlsdrkpadcvvtcdvqbqmwaaghiahtrpe---nfitssglqtm 403

Qy    412 ANALPIHIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKL 471
            |  :| | ||:  | :: :  :||||  :|: | :| |:  ::|:|:|:  :| :|||::
Db    404 gfglpaevgavqavarpndtvvcisgdgsfmmnvqelgtvkrkq1p1kivlldnqrlgmvrq 463

Qy    472 EMLVEGQPEFG----TDHEEVNFAEIAAAGIKSVRITDPPKKVREQLAEALAYPGPVLID 527
            :  : | | :      || : |   :|  |:    | |  ::  :   :|::  |  :::
Db    464 wcqlffgerysetttdnpd--fimlasafglhgqhitrkdqyeaaldtmlnsdgpyllh 521

Qy    528 IVTD 531
            :|:|
Db    522 vsid 525
```

```
XX
AC   R28618;
XX
DT   11-DEC-1992  (first entry)
XX
DE   Ala122 deleted acetohydroxy acid synthase.
XX
KW   AHAS; herbicide resistance; plants; imidazolinones;
KW   triazolopyrimidines; sulphonylureas.
XX
OS   Arabidopsis thaliana.
XX
PN   EP492113-A.
XX
PD   01-JUL-1992.
XX
PF   12-NOV-1991;  91EP-0119254.
XX
PR   27-DEC-1990;  90US-0633210.
XX
PA   (AMCY ) AMERICAN CYANAMID CO.
XX
PI   Chaleff RS, Hand JM, Singh BK;
XX
DR   WPI; 1992-218438/27.
XX
PT   Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT   nucleic acid sequences which can confer herbicide resistance to
PT   plants.
XX
PS   Claim 4; Page 20; 37pp; English.
XX
CC   The sequence is that of Ala122 deleted acetohydroxy acid synthase
CC   (AHAS) which is herbicide resistant. Transgenic plants may be
CC   produced which contain the modified gene and produce the Ala122
CC   deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC   The gene can thus be used to provide crop plants with resistance
CC   to herbicides such as imidazolinones, triazolopyrimidines and
CC   sulphonylureas. See also R24798-R24801 and R28609-R28624.
XX
SQ   Sequence   669 AA;

Query Match     16.6%;   Score 496.5;   DB 13;   Length 669;
Best Local Similarity     27.4%;   Pred. No. 4.2e-34;
Matches 157;   Conservative 96;   Mismatches 261;   Indels 59;   Gaps 13;

Qy      6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQSDIEWVHVRNEEAAAFAAGAESLITGE 65
            | :|   | :||| : ||        :||:|    :|::   |       | |:|   ||
Db    100 adilveaicrqgvtetvfayppgysmeihqaltrssslrnvlprheqgvfaaegyarssgk 159

Qy     66 LAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSG 125
            |   :|:||| |||   ||| |    | |:| ::: |   :||:|:|| |    :   : |
Db    160 pgiciatspgathlsvglladallsvplvaitgqvprrmigtdafqetplvevtrsitk 219

Qy    126 YCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVV 184
              : : :   | |:|  :  :: | :  | :|: |      :   :     :|   ||
Db    220 hnyivmdvediprilaeaffiatsgrppvlvdvpkdi-qgqlalpnweqamrlppyymsr 278

Qy    185 FPDPTEAAAL---VEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYIQ 241
            :|       |   ||  :  |:       | : : | :: |   |  |  :||||  :
Db    279 mpkppedshleqivrllseskkpvlyvgggclnssdelgrfveltcqipvastlmqlgsyp 338

Qy    242 HENPFEVGMSGLLGYGACVDASNEADLLILLGTDF------PYSDFLPKDNVAQVDINGA 295
             :: :  ||  :  | ||:   :: :||:: |:||       |  ::    :  :||  |
Db    339 cddelslhnlgmhgtvyanyavehsdllafgvrfddrvtgkleafasrakivhidisa 398

Qy    296 HIGRRTTVKYPVTGDVAATIENILPHVKEKTDRSFLDRML--KAHERKLSSVVETYTHNV 353
            :|  ::  :        :| :  :|       | ::::     :  ::| |    : |:|
Db    399 eignknktphvsvcgdvklalqg-----------mnkvlenraeelkldfgvwrnelnv 445

Qy    354 EKH-------VPIHPEYVASILNELADKDAVFTVDTGMCNVWHARYIENPEGTRDFV 403
            :|         :| : |  :
Db
```

```
RESULT  10
ID   R28618   standard; protein; 669 AA.
```

```
Db   446 qkqkfplsfktfgeaippqyalkvldeltgkaiistgvgqhqmwaaqfy-nykkprqwl 504
             ||||   |     ||| |  |||   |  ||:    :|:  |||||||
Qy   404 GSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLLGMLLGELLTVKLHQLPLKAVVFNN 463
         ||       |:::|||||| |||  |  |  :|| |:|     ||::| |||   ||||||
Db   505 sssgglgamgfglpaaigasvanpdaivdldgdgsfimnvqelatirvenlpvkvlllnn 564
         ::|||||| |||| ||||||    |    |  |||||         :| || ||| :||
Qy   464 SSLGMVKLEMLVE----------GQPEFGTDHEEV--NFAEIANAAGIKSVRITDPK 508
         :|||||:|:              ||||||||||||   ||||  ||||||||||||
Db   565 qhlgmv---mqwedrifykanrahtfigdp--aqedeifpmllfaaacgipaarvtkka 618
           :|| ||        :|  |  |  ||    || :||||||||||||| |||  | |
Qy   509 KVREQLAEALAYPGPVLIDIVTDPNALSIPPTI 541
          :  |:||||||||||||||||||||||||||
Db   619 dlreaiqtmldtpgpyllidvic-phqehvlpmi 650
```

```
RESULT 11
XX
ID    R24798 standard; Protein; 669 AA.
XX
AC    R24798;
XX
DT    11-DEC-1992 (first entry)
XX
DE    Trp574 deleted acetohydroxy acid synthase.
XX
KW    AHAS; herbicide resistance; plants; imidazolinones;
KW    triazolopyrimidines; sulphonylureas.
XX
OS    Arabidopsis thaliana.
XX
PN    EP492113-A.
XX
PD    01-JUL-1992.
XX
PF    12-NOV-1991;    91EP-0119254.
XX
PR    27-DEC-1990;    90US-0633210.
XX
PA    (AMCY ) AMERICAN CYANAMID CO.
XX
PI    Chaleff RS, Hand JM, Singh BK;
XX
DR    N-PSDB: Q26001.
XX
PT    nucleic acid sequences which can confer herbicide resistance to
PT    Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT    plants
XX
CC    The sequence is that of Trp574 deleted acetohydroxy acid synthase
CC    (AHAS) which is herbicide resistant. Transgenic plants may be
CC    produced which contain the modified gene and produce the Trp574
CC    deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC    The gene can thus be used to provide crop plants with resistance
CC    to herbicides such as imidazolinones, triazolopyrimidines and
CC    sulphonylureas.  See also R24797 and R24801.
XX
Example; Page 8; 37pp; English.
XX
SQ    Sequence    669 AA;

Query Match    16.68%;    Score 495.5;    DB 13;    Length 669;
Best Local Similarity    27.5%;    Pred. No. 5.1e-34;
Matches  157;    Conservative  97;    Mismatches 263;    Indels  53;    Gaps  13;

Qy     6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAV--RQSDIEWHVHVRNEEAAAFAAGAESLITG 64
         :|:|| |||::||||  :|: |   |:|:|   |  | :|:|   |  ||:    || :   :|: ||
Db   100 adilvealerggvetvfayppgqasmeihqaltrsssirnvlprheggyvfaaegyarssg 159
Qy    65 ELAVCAASCGPGNTHLIGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECS 124
         :|: ||  ||   :||: | |   |:: | || | :|   |:: : | |   | | |||  :
Db   160 kpgiciatsgpgatnlvsgladalldsvplvaitgqvprrmigtdafqetpivevtrsit 219
```

```
Qy   125 GYCEMVNGGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPV 183
         : |:              |    || |  | |||    | :| |  ||::       |||
Db   220 khnylvmdvedilprieeafflatsgtpgpplvdvpkdi-qgqlaipnweqamrlpgyms 278
Qy   184 VFPDPTEAAAL--VERAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYI 240
         :|:|           :|  |||  |  :|||| |::|  |||  |  :|||  | |||:||
Db   279 rmpkppedshleqivrliseskkpvlyvgggclnssdelgrfveltgipvastilmglgsy 338
Qy   241 QHENPFEVGMSGLLGYGACVDASNEADLLILLGTDF-----PYSDFLPKDNVAQVDING 294
          :|:||| ||||| |  | : |  | ||||| ||||     |::|  |  |:||:|:
Db   339 pcddelslhmlgmhgtvyanyavehsdllafgvrfddrvtgkleafasrakivhidis 398
Qy   295 AHIGRRTTVKIYPVTGVAATIENILPHVKEKIDRSFLDRML--KAHERKLSSVVETYTHN 352
          :|:|  :   :    :|  |  ||   |::  |     ||   :  |:  |  ||:|
Db   399 aeigknktphvsvcgdvklalgg------------mnkvlenraeelkldfgvwrneln 445
Qy   353 VEKH---------VPIHPEYVASILNELADKDAVFIVDTGMCNVWHARYIENPEGTRDF 402
         | :|          |:|| |  |::|||| | | |:|| ||    ||||::||  || |
Db   446 vqkqkfplsfktfgeaippqyaikvldeltdgkaiistgvgqhqmwaaqfy-nykkprqw 504
Qy   403 VGSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLLGMLLGELLTVKLHQLPLKAVVFN 462
         :   ||   | |:::|||||| |||  |  |  :|| |:|     ||::| |||   ||||
Db   505 lsssgglgamgfglpaaigasvanpdaivdldgdgsfimnvqelatirvenlpvkvlln 564
Qy   463 NSSLGMVKLE--------MLVEGQPEFGTDHEEV--NFAEIAAAAGIKSVRITDPKKVR 511
         |:||||:|:          :  ||||||||||||   ||||  |||||||||||||  :|
Db   565 nqhlgmvmqwedrifykanrahtfigdp--aqedeifpmllfaaacgipaaritkkadir 621
Qy   512 EQLAEALAYPGPVLIDIVTDPNALSIPPTI 541
          :  |:||||||||||||||||||||||||
Db   622 eaiqtmldtpgpyllidvic-phqehvlpmi 650
```

```
RESULT 12
XX
ID    R28617 standard; Protein; 669 AA.
XX
AC    R28617;
XX
DT    11-DEC-1992 (first entry)
XX
DE    Gly121 deleted acetohydroxy acid synthase.
XX
KW    AHAS; herbicide resistance; plants; imidazolinones;
KW    triazolopyrimidines; sulphonylureas.
XX
OS    Arabidopsis thaliana.
XX
PN    EP492113-A.
XX
PD    01-JUL-1992.
XX
PF    12-NOV-1991;    91EP-0119254.
XX
PR    27-DEC-1990;    90US-0633210.
XX
PA    (AMCY ) AMERICAN CYANAMID CO.
XX
PI    Chaleff RS, Hand JM, Singh BK;
XX
DR    WPI; 1992-218438/27.
XX
PT    nucleic acid sequences which can confer herbicide resistance to
PT    Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT    plants
XX
Claim 4; Page 20; 37pp; English.
XX
CC    The sequence is that of Gly121 deleted acetohydroxy acid synthase
CC    (AHAS) which is herbicide resistant. Transgenic plants may be
CC    produced which contain the modified gene and produce the Gly121
CC    deleted AHAS in the presence of an inhibitory amt. of herbicide.
```

```
CC   The gene can thus be used to provide crop plants with resistance
CC   to herbicides such as imidazolinones, triazolopyrimidines and
CC   sulphonylureas. See also R24798-R24801 and R28609-R28624.
XX
SQ   Sequence    669 AA;
```

```
Query Match             16.6%;  Score 495.5;  DB 13;  Length 669;
Best Local Similarity   27.4%;  Pred. No. 5.1e-34;
Matches  157;  Conservative  96;  Mismatches  261;  Indels  59;  Gaps  13;

Qy       6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVYRQSDIEWVHVRNEEAAAFAAGAESLITGE  65
           ::|:::|:||  |||::|:||:||:||||||:  ::|:||||||||||  |:||||||||
Db     100 adilvealerggvetvfayppgasmeihgaltrsssirnvlprheqgyvfaaegyarssgk 159

Qy      66 LAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECSG  125
           |||:|| :|||||||||||:||||||||||||||:|||||||||||||||||||:|||:|
Db     160 pgiciatsgppgatnlvsgladalldsvplivaltgqvprrmigtdafqetpivevtrsitk 219

Qy     126 YCEMVNGCGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPVV 184
           |::|:||| ||:|||||:|||:||||| ||:||||||:||:|:||||:||:|||:|||:
Db     220 hnylivmdvediprlieeafflatsgrppvlvdvpkdi-qqqlalpnweqamrlpgymsr 278

Qy     185 FPDPPTEAAAL.--VEAINNAKSVTLFCGGAGVKNARAQVLELAEKIKSPIGHALGGKQYIQ 241
           :::|||||||  :||:|::|| :|:::||:|||||:|||:||||||||:||||:|||||:|
Db     279 mpkppedshleqivrllseskpvlyyggcclnssdelgrfveltgipvastlmglgsyp 338

Qy     242 HENPFEVGMSGLLGYGACVDASNEADLLILLGTDF------PYSDFLPKDNVAQVDINGA 295
           ::|||||||||||||||||||||||:|||||||||      |||||||||||||||||:|
Db     339 cddelslhmlgmhgtvyanyavehsdlllafgvrfddrvtgkleafasrakivhididsa 398

Qy     296 HIGRRTTVKYPVTGDVVAATIENILPHVKEKTDRSFLDRML--KAHERKLSSVVETYTHNV 353
           |::|||:||:|||| :::|:::|||:|||:||||||||||  :|||||||:||:||||||
Db     399 elgkknktphvsvcgdvklaigg------mnkvlenraeelkldfgvwrnelnv 445

Qy     354 EKH--------------VPIHPEYVASILNELADKDAVFTVDTGMCNVWHARYIENPEGTRDFV 403
           |||              ||||||||||||||||||||||||||||||||||||||||||:|||
Db     446 qkqkfplsfktfgeaippqyaikvldeltdgkalistgvghqmwaaqfy-nykkprqwl 504

Qy     404 GSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNN 463
           |||:||:||||||||||:||||:||||::|:||||:|:|||||||:|||||||||||::||
Db     505 sssgglgamgfglpaalgasvanpdaivvddigdgdsflmnvqelatirvenlpvkvll nn 564

Qy     464 SSLGMVKLEMLVE----------------GQPEFGTDHEEV--NFAEIAAAAGIKSVRITDPK 508
           ||||::||::||                 ||||:|||||||  ||||||||||||:|||||||
Db     565 qhlgmv---mqwedrfykanrahtfigdp---aqedeifpnmllfaaacglpaarvtkka 618

Qy     509 KVREQLAEALAYPGPVLIDIVTDPNALSIPPTI 541
           |:||||||||||||||||||||||||||||||||
Db     619 dlrealqtmldtpgpyylldvic-phqehvlpml 650
```

```
RESULT 13
R28623
ID   R28623 standard; protein; 669 AA.
XX
AC   R28623;
XX
DT   11-DEC-1992  (first entry)
XX
DE   Val571 deleted acetohydroxy acid synthase.
XX
KW   AHAS; herbicide resistance; plants; imidazolinones;
KW   triazolopyrimidines; sulphonylureas.
XX
OS   Arabidopsis thaliana.
XX
PN   EP492113-A.
XX
PD   01-JUL-1992.
XX
PF   12-NOV-1991;  91EP-0119254.
XX
```

```
PR   27-DEC-1990;  90US-0633210.
XX
PA   (AMCY ) AMERICAN CYANAMID CO.
XX
PI   Chaleff RS, Hand JM, Singh BK;
XX
DR   WPI; 1992-218438/27.
XX
CC   Claim 4; Page 20; 37pp; English.
XX
CC   The sequence is that of Val571 deleted acetohydroxy acid synthase
CC   (AHAS) which is herbicide resistant. Transgenic plants may be
CC   produced which contain the modified gene and produce the Val571
CC   deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC   The gene can thus be used to provide crop plants with resistance
CC   to herbicides such as imidazolinones, triazolopyrimidines and
CC   sulphonylureas. See also R24798-R24801 and R28609-R28624.
XX
SQ   Sequence    669 AA;
```

```
Query Match             16.6%;  Score 495.5;  DB 13;  Length 669;
Best Local Similarity   27.4%;  Pred. No. 5.1e-34;
Matches  156;  Conservative  99;  Mismatches  262;  Indels  53;  Gaps  13;

Qy       6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAV-RQSDIEWVHVRNEEAAAFAAGAESLITG 64
           ::|:::|:||  |||::|:||:||:||||||| :::|:||||||||||:  |:||||||||
Db     100 adilvealerggvetvfayppgasmeihgaltrsssirnvlprheqgyvfaaegyarssg 159

Qy      65 ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECS 124
           :|||:|| :|||||||||||:||||||||||||||:|||||||||||||||||:||||:|
Db     160 kpgiciatsgppgatnlvsgladalldsvplivaltgqvprrmigtdafqetpivevtrsit 219

Qy     125 GYCEMVNGCGEQGERILHHAIQSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPV 183
           |:::|:||| ||:|||||:|||:||||| ||:||||||:||:|:||||:||:|||:|||:|
Db     220 khnylivmdvediprlieeafflatsgrppvlvdvpkdi-qqqlalpnweqamrlpgyms 278

Qy     184 VFPDPPTEAAAL.--VEAINNAKSVTLFCGGAGVKNARAQVLELAEKIKSPIGHALGGKQYI 240
           :::::|||||||  :||:|::|| :|:::||:|||||:|||:||||||||:||||:||||||
Db     279 rmpkppedshleqivrllseskpvlyyggcclnssdelgrfveltgipvastlmglgsy 338

Qy     241 QHENPFEVGMSGLLGYGACVDASNEADLLILLGTDF------PYSDFLPKDNVAQVDING 294
           |::|||||||||||||||||||||||:|||||||||      ||||||||||||||||:
Db     339 pcddelslhmlgmhgtvyanyavehsdlllafgvrfddrvtgkleafasrakivhidids 398

Qy     295 AHIGRRTTVKYPVTGDVVAATIENILPHVKEKTDRSFLDRML--KAHERKLSSVVETYTHN 352
           :|::|||:||:|||| :::|:::|||:|||:||||||||||  :|||||||:||:|||||
Db     399 aelgkknktphvsvcgdvklaigg------mnkvlenraeelkldfgvwrneln 445

Qy     353 VEKH--------------VPIHPEYVASILNELADKDAVFTVDTGMCNVWHARYIENPEGTRDF 402
           |||              ||||||||||||||||||||||||||||||||||||||||||:||
Db     446 vqkqkfplsfktfgeaippqyaikvldeltdgkalistgvghqmwaaqfy-nykkprqw 504

Qy     403 VGSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFN 462
           |||:||:||||||||||:||||:||||::|:||||:|:|||||||:||||||||||::||
Db     505 lsssgglgamgfglpaalgasvanpdaivvddigdgdsflmnvqelatirvenlpvkvll 564

Qy     463 NSSLGMVKLE----------------MLVEGQPEFGTDHEEV--NFAEIAAAAGIKSVRITDPKKVR 511
           |||||::||                 |:||||||:|||||||  ||||||||||||:|||||||||
Db     565 nqhlgmvmqwedrfykanrahtfigdp---aqedeifpnmllfaaacglpaarvtkkadlr 621

Qy     512 EQLAEALAYPGPVLIDIVTDPNALSIPPTI 541
           |||||||||||||||||||||||||||||||
Db     622 eaiqtmldtpgpyylldvic-phqehvlpml 650
```

```
RESULT 14
R28616
ID   R28616 standard; protein; 666 AA.
```

XX
AC   R28616;
XX
DT   11-DEC-1992 (first entry)
XX
DE   Amino acids 650-653 deleted acetohydroxy acid synthase.
XX
KW   AHAS; herbicide resistance; plants; imidazolinones;
KW   triazolopyrimidines; sulphonylureas.
XX
OS   Arabidopsis thaliana.
XX
PN   EP492113-A.
XX
PD   01-JUL-1992.
XX
PF   12-NOV-1991; 91EP-0119254.
XX
PR   27-DEC-1990; 90US-0633210.
XX
PA   (AMCY) AMERICAN CYANAMID CO.
XX
PI   Chaleff RS, Hand JM, Singh BK;
XX
DR   WPI; 1992-218438/27.
XX
PT   Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT   nucleic acid sequences which can confer herbicide resistance to
PT   plants
XX
CC   The sequence is that of amino acids 650-653 deleted acetohydroxy acid
CC   synthase (AHAS) which is herbicide resistant. Transgenic plants may be
CC   produced which contain the modified gene and produce the 650-653
CC   deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC   The gene can thus be used to provide crop plants with resistance
CC   to herbicides such as imidazolinones, triazolopyrimidines and
CC   sulphonylureas. See also R24798-R24801 and R28609-R28624.
XX
SQ   Sequence   666 AA;

Query Match   16.6%;   Score 495;   DB 13;   Length 666;
Best Local Similarity   27.4%;   Pred. No. 5,6e-34;
Matches 159;   Conservative 99;   Mismatches 262;   Indels 60;   Gaps 14;

```
Qy      6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAV-RQSDIEWVHVRNEEAAAFAAGAESLITG 64
          : |:| ||| :  |  |:| ||| ||:|:|| |: :||  ||| ||:: ::|: : |:|
Db    100 adilvealerqgvetvfayppgasmeihgaltrsssirnvlprheggvfaaegyarssg 159

Qy     65 ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECS 124
          ||||| |:||||||||| |||| ||||||||||| ||||||||||||||||||||||||
Db    160 kpgiciatsgpgatnlvsgladalidsvplvaitgqvprmigtdafqetpivevtrsit 219

Qy    125 GYCEMVNGGEQGERILHHAIOSTMAGK-GVSVVVIPGDIAKEDAGDGTYSNSTISSGTPV 183
          | |  :  |:||| :  |  :|  |:| |: ||| | |:|:   | :|:|  |  |:
Db    220 khnyivmdvedipriieeafflatsgrpgpvivdvpkdi-qqqlaipnweqamrlpgyms 278

Qy    184 VFPDPTEAAAL---VEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYI 240
          :|  |  | |      | :: ||:  | | |     |  || | ::| || ||  |  :
Db    279 rmpkppedshleqivrlliseskkpvlyvgggcInssdelgrfveltgipvastlmglgsy 338

Qy    241 QHENPEVGMSGLLGYGACVDASNEADLLILLGTDF------PYSDFLPKDNVAQVDING 294
          : | |: |  | | |  || ||: ||:|::|||         | : ||:||| |: | |
Db    339 pcddelslhmlgmhgtvyanyavehsdllafgvrfddrvtgkleafasrakivhidids 398

Qy    295 AHIGRRTTVKYPVTGDVAAITENILPHVKEKTRDRSFLDRML--KAHERKLSSVVEYTHN 352
          |  |  | |  :: | :|   |::| | |  |:|  |:|      ||  |:|  |  ||:
Db    399 aeigknktphvsvcgdvklaigg-------mkvlenraeelkldfgvwrneln 445

Qy    353 VEKH--------VPIHPEYVASILNELADKDAVFTVDIGMCNVWHARIIENPEGTRDF 402
          :|       :||| | :  || :| | | |  | | | :  |    |  | : :||
Db    446 vqkqkfplsfktfgealppqyaikvldeltdgkalistgvghqmwaaqfy-nykprqw 504

Qy    403 VGSFRHGTMANALPHAIGAQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPKAVVFN 462
          ||:  ||| ||  |  | |  | | | |: |||||| |||| |||| ||: ||: | |
Db    505 lssgglgamgfglpaailgasvanpdaivdigdgsfimnvgelatirvenlpvkvllln 564

Qy    463 NSSLGMVKLEMLVE-----------GQPEFGTDHEEV--NFAEIAAAGIKSVRITDP 507
          |  ||||    |    :     |::  | : |  ||      |:||||| | | |:|
Db    565 nqhlgmv---mgwedrfykanrahtflgdp--aqedeifpomllfaaacglpaarvtkk 618

Qy    508 KKVREQLAEALATPGPVLIDIVTDPNALSIPPPITWEGQVM 547
          |  |||| | | ||||| :|:|   ||:| |:| :  |::|
Db    619 adlrealqtmldtpgpylldvic-phqehvlpggtfndvi 657
```

RESULT 15
ID   R28624 standard; Protein; 669 AA.
XX
AC   R28624;
XX
DT   11-DEC-1992 (first entry)
XX
DE   Phe578 deleted acetohydroxy acid synthase.
XX
KW   AHAS; herbicide resistance; plants; imidazolinones;
KW   triazolopyrimidines; sulphonylureas.
XX
OS   Arabidopsis thaliana.
XX
PN   EP492113-A.
XX
PD   01-JUL-1992.
XX
PF   12-NOV-1991; 91EP-0119254.
XX
PR   27-DEC-1990; 90US-0633210.
XX
PA   (AMCY) AMERICAN CYANAMID CO.
XX
PI   Chaleff RS, Hand JM, Singh BK;
XX
DR   WPI; 1992-218438/27.
XX
PT   Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by
PT   nucleic acid sequences which can confer herbicide resistance to
PT   plants
XX
CC   The sequence is that of Phe578 deleted acetohydroxy acid synthase
CC   (AHAS) which is herbicide resistant. Transgenic plants may be
CC   produced which contain the modified gene and produce the Phe578
CC   deleted AHAS in the presence of an inhibitory amt. of herbicide.
CC   The gene can thus be used to provide crop plants with resistance
CC   to herbicides such as imidazolinones, triazolopyrimidines and
CC   sulphonylureas. See also R24798-R24801 and R28609-R28623.
XX
SQ   Sequence   669 AA;

Query Match   16.6%;   Score 494.5;   DB 13;   Length 669;
Best Local Similarity   27.5%;   Pred. No. 6.2e-34;
Matches 157;   Conservative 99;   Mismatches 261;   Indels 53;   Gaps 13;

```
Qy      6 AEQLIDTLEAQGVKRIYGLVGDSLNPIVDAV-RQSDIEWVHVRNEEAAAFAAGAESLITG 64
          : |:| ||| :  |  |:| ||| ||:|:|| |: :||  ||| ||:: ::|: : |:|
Db    100 adilvealerqgvetvfayppgasmeihgaltrsssirnvlprheggvfaaegyarssg 159

Qy     65 ELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILFKECS 124
          ||||| |:||||||||| |||| ||||||||||| ||||||||||||||||||||||||
Db    160 kpgiciatsgpgatnlvsgladalidsvplvaitgqvprmigtdafqetpivevtrsit 219
```

```
Qy   125  GYCEMVNGGEQGEERILHHAIQSTMAGK-GVSVVVIPGDIAKEDACGDGTYSNSTISSGTPV  183
             .:     :::  ::   :.  | |||   |  ::
Db   220  khnylvndvedlprileeafflatsgrpgpvlvdvpkdl-qgqlalpnweqamrlpgyms   278

Qy   184  VFPDPTEAAAL---VEAINNAKSVTLPCGAGVKNARAQVLELAEKIKSPIGHALGGKQYI   240
            |  |         ::  ||  |  | :: :   |     ::
Db   279  rmpkppedshleqivrliseskkpvlyvgggclnssdelgrfveltgipvastlmglgsy  338

Qy   241  QHENPFEVGMSGLLGYGACVDASNEADLLILLGTDF-----PYSDFLPKDNVAQVDING    294
            ::    :  :                  ::::||
Db   339  pcddelalhmlgmhgtvyanyavehsdlliafgvrfddrvtgkleafasraklvhidlds  398

Qy   295  AHIGRRTTVKYPVTGDVAATIENILPHVKEKTDRSFLDRML--KAHERKLSSVVETYTHN   352
            |||  | |  | |  ||      :::::|  | |   |       |
Db   399  aelgknktphvsvcgdvklalgg--------mnkvlenraeelkldfgvwrneln       445

Qy   353  VEKH--------VPIHPEYVASILNELADKDAVFTVVDTGMCNVWHARYIENPEGTRDF    402
            | :         :|:                       :
Db   446  vqkqkfplsfktfgealppqyalkvldeltdgkailstgvgghqmwaaqfiy-nykkprqw 504

Qy   403  VGSFRHGTMANALPIIAIGAQSVDRNRQVIAMCGDGGILGMLLGELLTVKLHQLPLKAVVFN 462
            :    | ||  |  :   |  |   :  ||    |||||     |   :  ||  |
Db   505  lssgglgamgfglpaalgasvanpdalvvdidgdgsflmnvqelatirvenlpvkvllln   564

Qy   463  NSSLGMVKLEMLVEGQPEFGTDH----------EEV--NFAEIAAAGIKSVRITDPKKVR   511
            :  ||||     || |||    :       :  ::::     |  |:|   :   :|
Db   565  nqhlgmv---mqwedrykanrahtflgdpaqedelfpnmllfaaacglpaarvtkkadlr  621

Qy   512  EQLAEALAYPGPVLIDIVTDPNALSIPPTI  541
            |  |     |  :||:||:|::|  | |  |
Db   622  eatqtmldtppyvldvic-phqehvlpml   650
```

Search completed: March 17, 2001, 21:51:02
Job time: 5109 sec

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